



Estimation of genetic variability and association between different yield components at seedling stage under water stress condition

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General Note

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ABSTRACT

Drought is the major abiotic stress responsible for yield losses in maize crop across the globe. In this study, fifty maize genotypes were evaluated for drought tolerance. All genotypes were statistically different from each other for all the studied physio-morphological parameters. Maximum fresh root length and fresh shoot length were recorded for OH-8 and OH-54-3A maize genotypes respectively while maximum fresh root weight and dry root weight were attained by A556 and WMA13RA respectively. Fresh shoot weight, fresh root weight, fresh biomass, dry shoot weight and dry root weight had positive and significant correlation

with dry biomass at genotypic level. Whereas, dry shoot weight had significant positive association with fresh shoot weight, fresh root weight and fresh biomass at genotypic level. All the characters under studied showed high estimates of heritability however fresh shoot length, fresh root length and fresh biomass showed high genetic advance. The results of heritability and genetic advance studies suggested that yield in maize genotypes can be increased under drought stress by selection for fresh shoot weight, shoot and root length and fresh biomass.

Keywords: Correlation, genetic advance, genotype, heritability, coefficient of variance, maize.

1. INTRODUCTION

Among cereals maize is the third most important grain crop around the globe, large population in Africa, Latin America, Caribbean and Asia consume maize as staple food. Maize crop is grown under diverse climatologically zones and its area is increasing due to its demand for industry, livestock and human consumption (FAO, 2015). In Pakistan maize occupies an impotent position to fulfill the needs of large poultry industry, cattle, wet milling industry and human consumption (Saleem *et al.* 2011). This need is fulfilled by two crops in a calendar year and water is the major limiting factor for yield loss (Mustafa *et al.* 2013). Most of the maize area in Pakistan falls under irrigated regions and availability of irrigation water is decreasing drastically by every passing year and underground water is also not fit for irrigation in most of the areas and present emerging climate change is another threat for sustainable crop production (Pakistan Economic Survey, 2014-15; Pabitra Aryal, 2015; Anthony Whitbread, 2015; Tushar Pandey, 2015).

Drought is an unavoidable and recurring feature of world agriculture among different abiotic stresses. It has been assessed that about one third of the world's potentially arable land suffers water scarcity and causes loss in crop yield (Mustafa *et al.* 2015; Ahmad Raza *et al.* 2017). Maize crop is sensitive to drought stress, normal photosynthesis decreases due to reduction of CO₂/O₂ ratio in leaves, reduced uptake of nutrients lead to hampered flowering, abnormal anthesis-silking interval and low grain yield (Taiz & Zeiger, 2006; Saif-ul-Malook *et al.* 2014). Less sensitive, well adapted maize germplasm can yield better under water stress environment. The efficiency of selection for drought tolerance can be increased by selection through the secondary traits (like anthesis-silking interval) with high correlation and heritability (Ziyomo and Bernardo, 2013). The relationship between two traits can directly be observed as phenotypic correlation while genotypic correlation coefficient express the extent to which two traits are genotypically associated (Yousaf and Saleem, 2001). The present study was designed keeping in view the current scenario of decreased availability of water and utilize those traits which can confer drought tolerance and contribute to yield stability under stress.

2. MATERIAL AND METHOD

The study was designed to investigate the genetic association of different seedling characters of maize genotypes planted at University College of Agriculture, University of Sargodha, Pakistan. Fifty genotypes were collected from different research organizations having diverse genetic base. These genotypes were planted in iron trays filled with sand (pH 7.8 and EC 1.7 dSm⁻¹) in three replications under completely randomized design. Moisture level was maintained on alternative days with the help of moisture meter at 50% field capacity. At the stage of five leaves, ten plants from each entry of each repeat were selected for data recording. Data for fresh root weight, dry root weight, fresh shoot weight and dry shoot weight, root shoot ratio, fresh shoot length, fresh root length fresh biomass and dry biomass were recorded. The recorded data were subjected to analysis of variance, phenotypic variances, heritability and genotypic variances. Genotypic and phenotypic correlation coefficients were calculated by techniques of Kohn and Torrie (1964). Genetic advance was estimated using the method given by Falconer, 1989.

3. RESULTS AND DISCUSSION

It is persuaded from Fig. 1 and 2 that higher fresh root length was recorded for OH-8, A509 and OH-54-3A while lower values have been recorded for WA3748 and 82P1 but higher fresh shoot length was recorded for OH-54-3A, OH-8 and A509 while lower for B34-2B and N48-1. The higher values of fresh shoot and root length indicated that lines A509 and OH-54-3A may be used to develop tolerant genotypes Ali *et al.* (2011, 2012).

Fresh Root Length

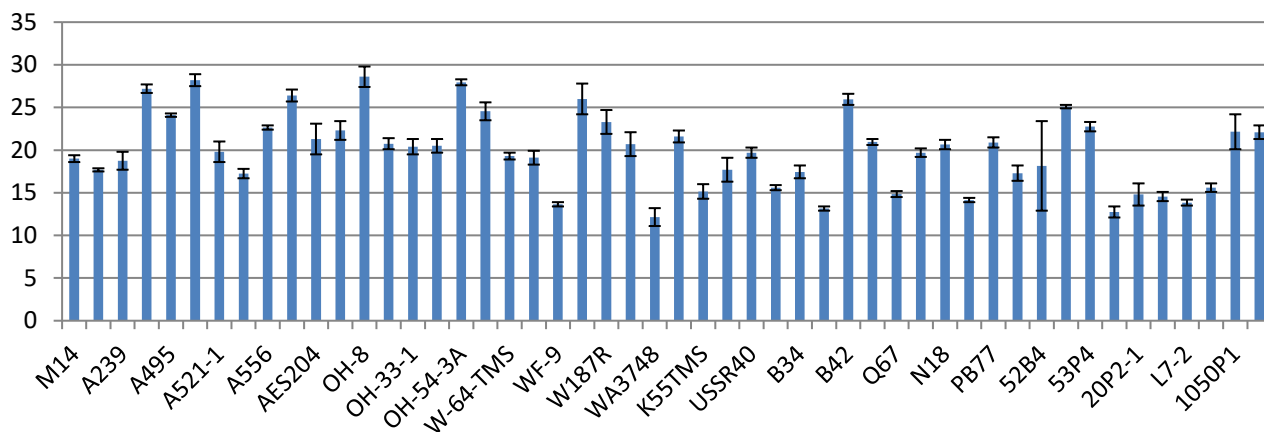


FIG. 1

Fresh Shoot Length

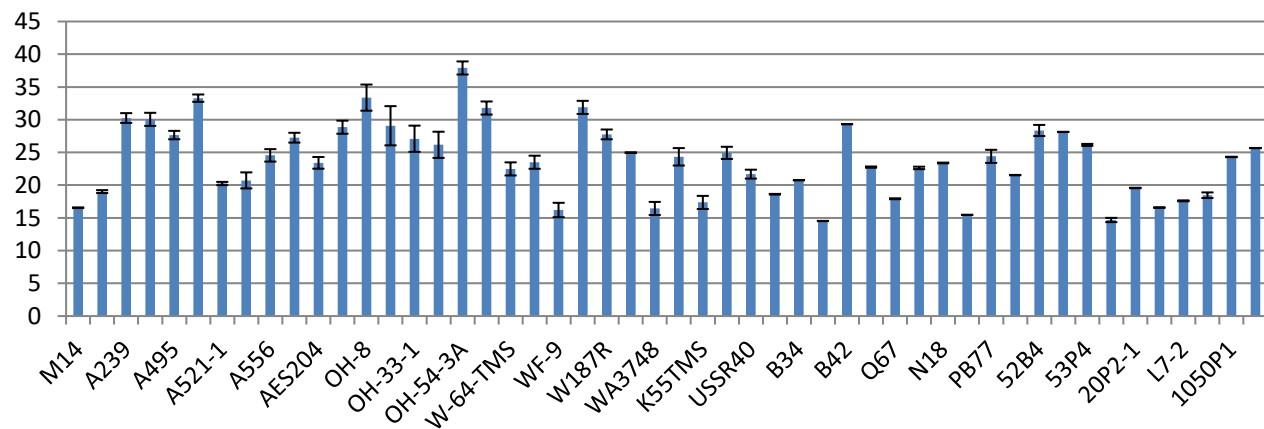


FIG. 2

Fig. 3 represented that genotypes/accessions A556 had maximum fresh root weight followed by A509 and WMA13RA while Q67 had minimum root weight followed by B34-2B. Genotypes/accessions WMA13RA showed maximum dry root weight followed by A509 (Fig. 4) while Q67 and A545 showed minimum value of dry root weight. The higher values of fresh and dry root weight of A509 and WMA13RA indicated that these genotypes/accessions may be selected to develop drought tolerant genotypes Ali *et al.* (2011, 2012) and Mustafa *et al.* (2014).

Fresh Root Weight

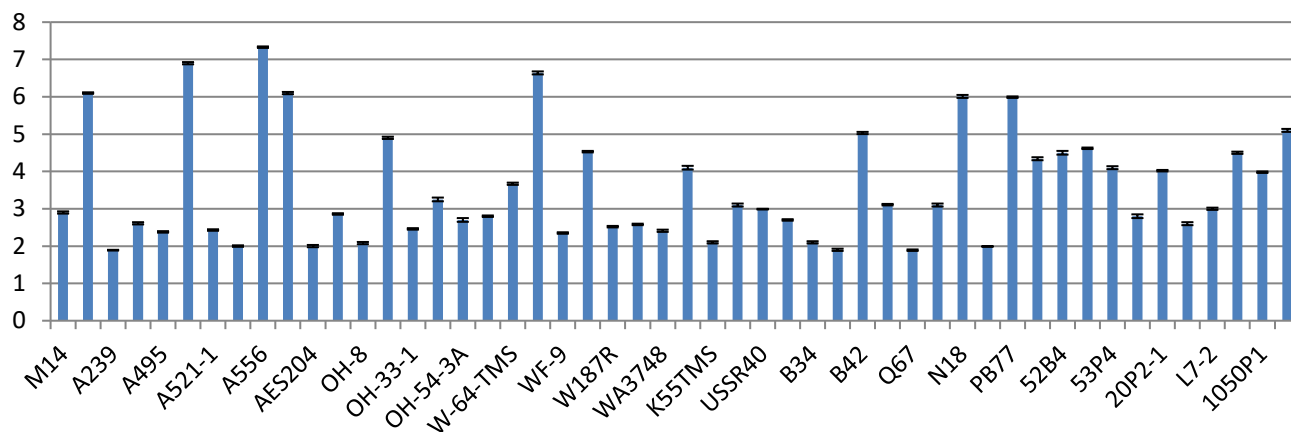


FIG. 3

Dry Root Weight

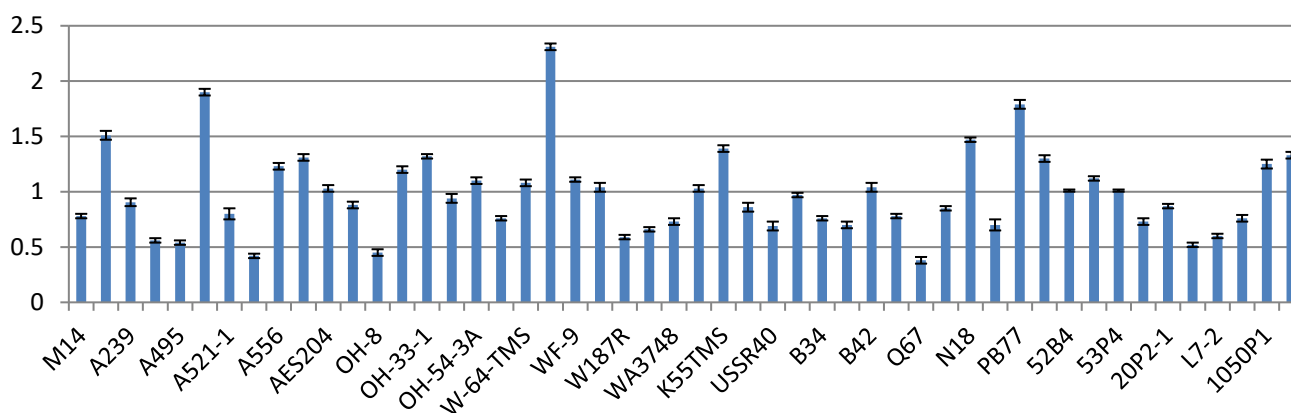


FIG. 4

It is clear from the Fig. 5 that genotypes/accessions A509, A556 and 150-2 had maximum fresh shoot weight while N48-1 had minimum fresh shoot weight. Genotypes/accessions A556 showed maximum dry shoot weight followed by AES204 (Fig. 6) while N48-1 showed minimum value of dry shoot weight. The higher values of fresh and dry shoot weights indicated that genotypes/accessions A509 and A556 may be used to develop drought tolerant genotypes Ali *et al.* (2011, 2012).

Fresh Shoot Weight

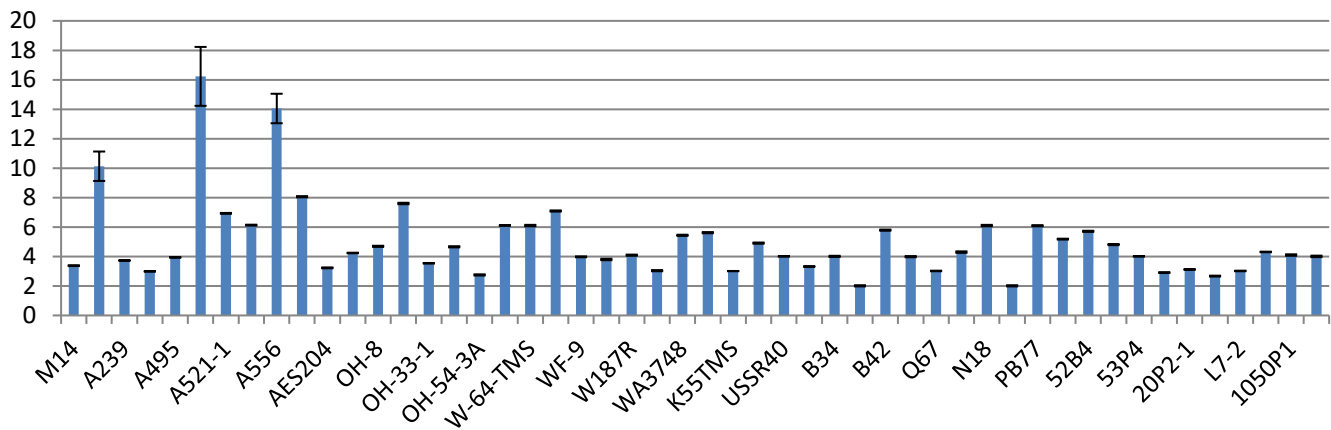


FIG. 5

Dry Shoot Weight

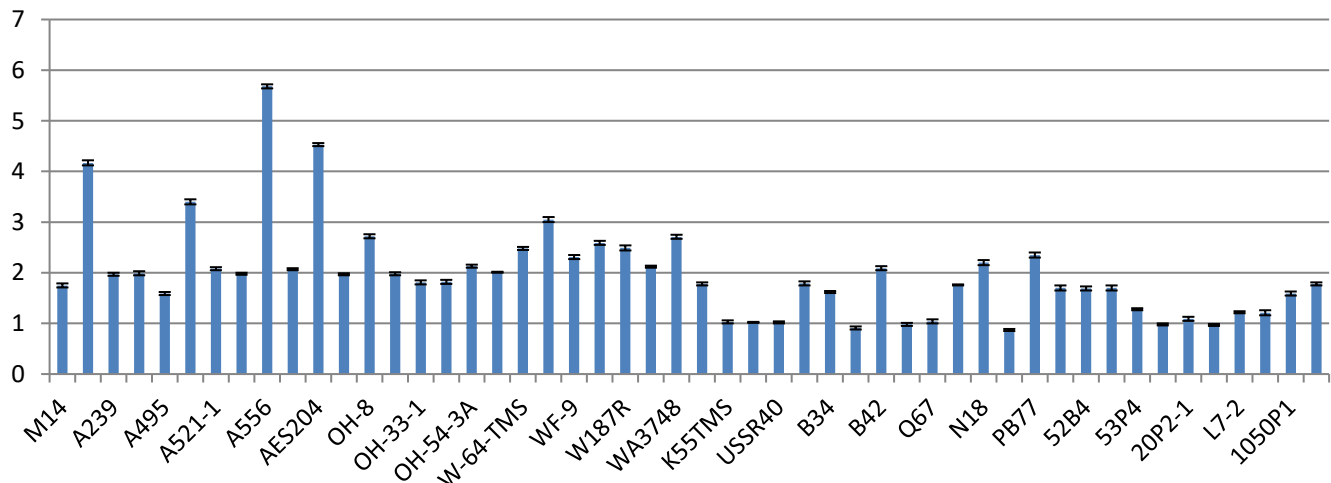


FIG. 6

It is indicated from Fig. 7 that genotypes WF-TMS and W-64-SP had maximum Stomata size while OH-41 had minimum stomata size. Higher values of stomata size represented by WF-TMS and W-64-SP may be used to develop high drought maize genotypes. Fig. 8 indicated that genotypes/accessions K55TMS and GPF-9 had higher root shoot ratio while OH-8 showed minimum root shoot ratio. Higher values of root shoot ratio indicated that K55TMS and GPF-9 may be selected for drought breeding program to develop new genotypes Ali *et al.* (2011, 2012).

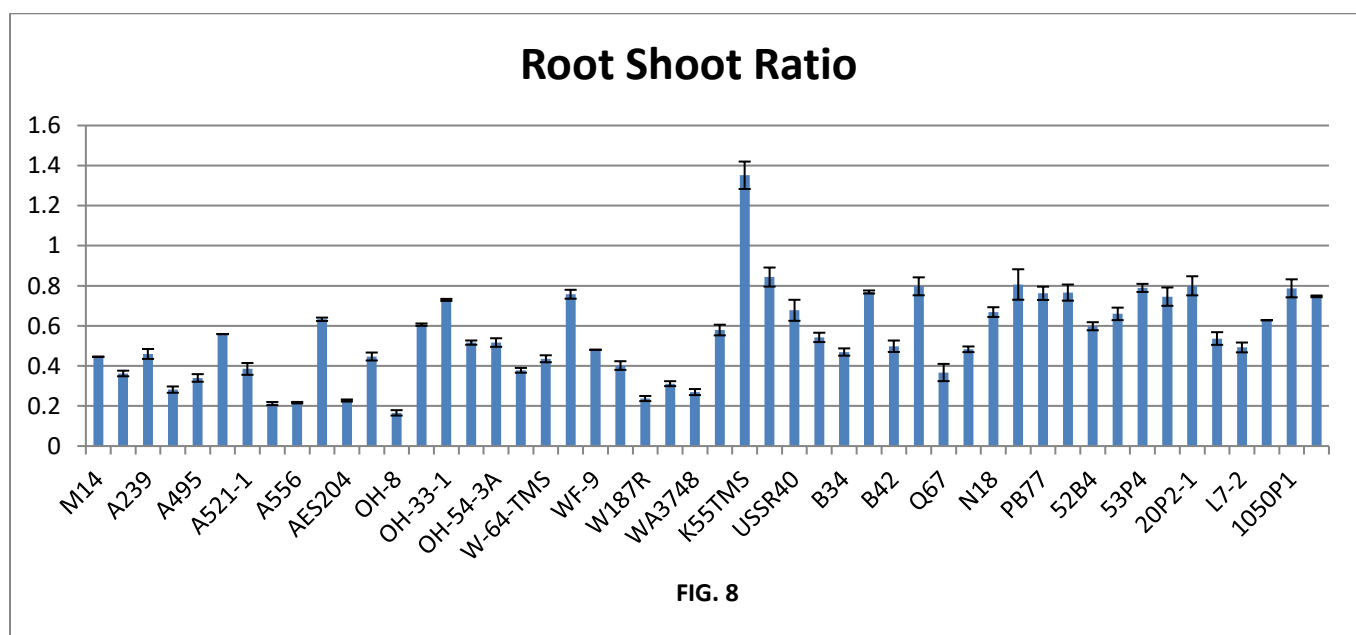
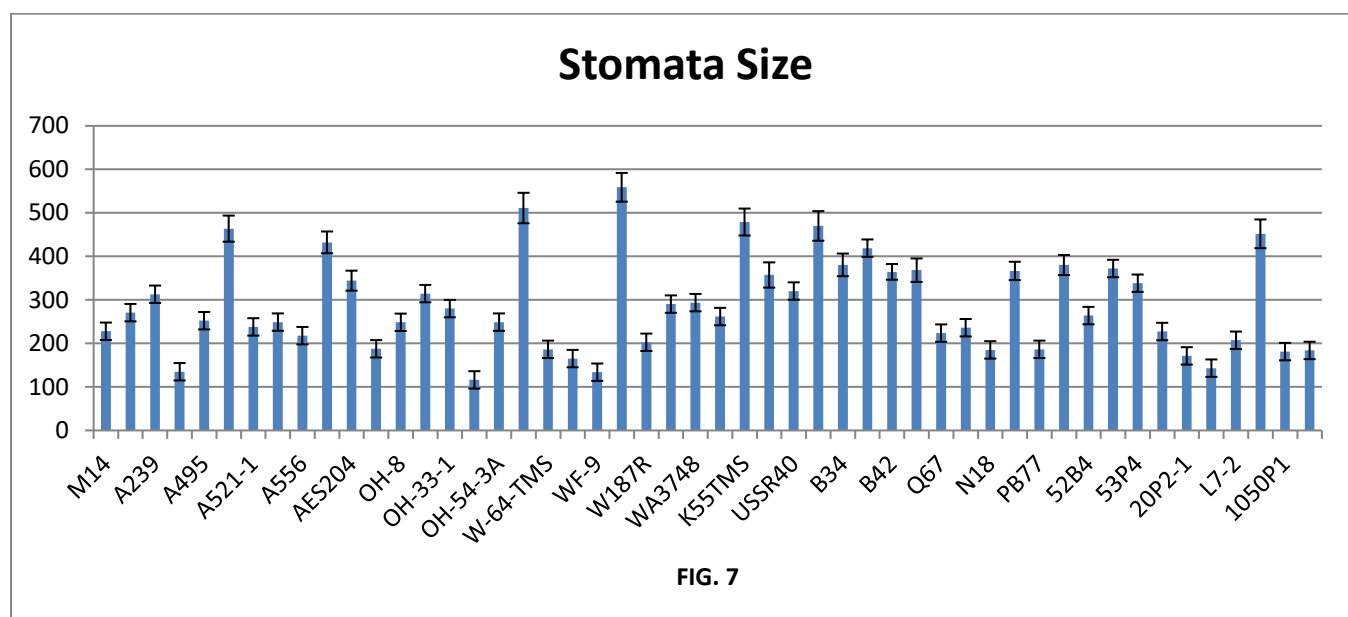


Fig. 9 indicated that genotypes/accessions A509, A556 and 150-2 had maximum values of fresh biomass while B34-2B and N48-1 had minimum values of fresh and dry biomass. Genotypes/accessions A556 and 150-2 showed maximum value of dry biomass (Fig. 10) while Q67 showed minimum value of dry biomass. So, higher values of A556, A509 and 150-2 for fresh and dry biomass indicated that these genotypes/accessions may be used to develop high yielding drought tolerant genotypes Ali *et al.* (2011, 2012).

Fresh Biomass

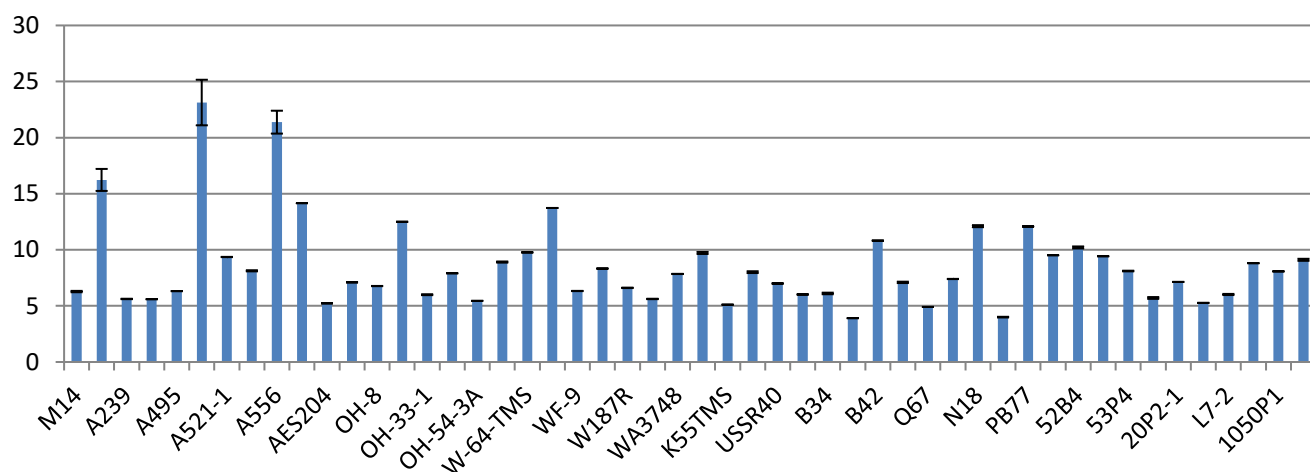


FIG. 9

Dry Biomass

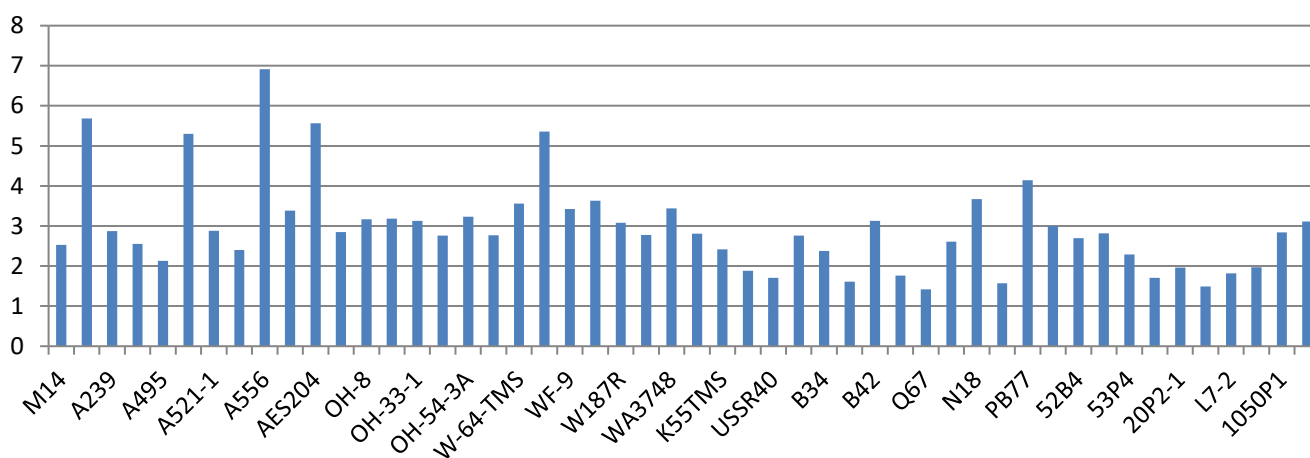


FIG. 10

It is clear from the table 1 that higher genotypic and phenotypic coefficient of variations were recorded for fresh shoot weight (53.18, 54.06) followed by dry shoot weight (47.22, 47.30) respectively while the lowest were recorded for fresh root length (21.15, 22.66). All the characters under studied showed high estimates of heritability however fresh shoot length, fresh root length and fresh biomass showed high genetic advance. Higher genetic advance and heritability indicated that selection for higher yielding maize genotypes for drought tolerance may be useful on the basis of fresh shoot weight, fresh shoot and root length and fresh biomass.

It is concluded from the study that fresh shoot length had positive and highly significant genotypic and phenotypic correlation with fresh shoot length while it had negative but non-significant correlation with root shoot ratio (Table 2). Fresh root length had positive but non-significant genotypic and phenotypic association with fresh shoot weight, fresh root weight, fresh biomass, dry shoot weight, dry root weight and dry biomass. Similar results were reported by Ali *et al.* (2013), Khan *et al.* (2004) and Ahsan *et al.* (2011). Strong genotypic association of fresh shoot length with fresh root length indicated that selection on the basis of these traits may be helpful to improve the yield of maize genotypes. Positive and significant genotypic and phenotypic associations were also

found between fresh root weight, fresh biomass, dry shoot weight, dry root weight and dry biomass. Fresh root weight was positively and significantly associated with fresh shoot weight, fresh biomass, dry root weight and dry biomass both at phenotypic and genotypic levels. Similar type of association among parameters was also reported by Ali *et al.* (2013), Saif-ul-malook *et al.* (2014) and Ahsan *et al.* (2011). Fresh biomass had significantly positive genotypic and phenotypic correlation with dry shoot weight, dry root weight and dry biomass. Positive and significant correlation suggested that fresh biomass increased as most of the compounds were accumulated in the seedlings that reflect the ability of roots to develop under drought condition (Lobell, 2011 and Saif-ul-Malook, 2014) whereas fresh biomass had negative genotypic and phenotypic correlation with root shoot ratio.

Table 1 Genetic parameters of various traits of maize under drought condition

	SD	GCV	PCV	GA	H ²
Fresh root weight	1.49	41.89	41.90	2.62	0.963
Dry root weight	0.38	39.19	39.45	0.67	0.999
Fresh shoot weight	2.64	53.18	54.06	4.55	0.987
Dry shoot weight	0.93	47.22	47.30	1.64	0.968
Fresh root length	4.22	21.15	22.66	6.92	0.997
Root shoot ratio	0.22	39.97	40.78	0.38	0.928
Fresh biomass	3.87	45.45	45.80	6.74	0.960
Dry biomass	1.15	38.81	38.85	2.01	0.984
Fresh shoot length	5.48	23.02	23.45	9.43	0.998

Table 2 Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients for different traits of maize genotypes

	FSL	FRL	FSW	FRW	FBM	RSR	DSW	DRW	DBM
FSL	1	0.9324**	0.2785	0.2476	0.2851	-0.2474	0.2875	0.1977	0.3001
FRL	0.8539**	1	0.3560	0.3417	0.3741	-0.2897	0.3734	0.2114	0.3745
FSW	0.2681	0.3235	1	0.7389**	0.9658**	-0.1946	0.6734**	0.5386*	0.7281**
FRW	0.2430	0.1943	0.5317*	1	0.8884**	0.1554	0.4626**	0.7566**	0.6295**
FBM	0.2271	0.3445	0.9650**	0.8817**	1	-0.0727	0.6369**	0.6582*	0.7384**
RSR	-0.2387	-0.2667	-0.1855	0.1499	-0.0702	1	-0.5392*	0.4079	-0.3024
DSW	0.2830	0.3493	0.6623*	0.4623*	0.6318*	-0.5338*	1	0.4144*	0.9528**
DRW	0.1941	0.1943	0.5317*	0.7500**	0.6520*	0.4133*	0.4085	1	0.6724*
DBM	0.2958	0.3498	0.7181**	0.6286*	0.7337**	-0.2957	0.9516**	0.6691*	1

FSL= Fresh shoot length, FRL= Fresh root length, FSW= Fresh shoot weight, FRW= Fresh root weight, FBM= Fresh biomass, RSR= Root shoot ratio, DSW= Dry shoot weight, DRW= Dry root weight, DBM= Dry biomass

Dry shoot weight and dry root weight had positive and significant correlation association with dry biomass at both genotypic and phenotypic level. The results also indicate that maize genotypes for drought tolerance may be selected on the basis of root weight (Ali *et al.* 2013, Ali *et al.* 2011 and Blum 1988). Strong and highest genotypic and phenotypic association of dry biomass with dry shoot weight indicated that selection on the basis of these characters may be helpful to improve the yield of maize genotypes. The significant genotypic associations of the characters indicated that selection of these traits can be helpful to improve the maize genotypes under stress condition. (Saleem *et al.* 2007, Ali *et al.* 2011 and Stamp *et al.* 1986).

4. CONCLUSION

It is concluded from the present investigation that strong phenotypic and genotypic association was found between fresh shoot length and fresh root length, fresh shoot weight and fresh biomass, fresh shoot weight and fresh root weight, fresh shoot weight and dry biomass, fresh root weight and dry root weight and dry shoot weight and dry biomass. Based on results it is suggested that root and shoot length, dry shoot weight and dry biomass may be helpful to select higher yielding maize genotypes for drought stress conditions.

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